FIGURE 1

Nucleotide and Amino Acid Sequences of Gene X

```
aagccctgaa gggtcaaaag aaatacaaaa gcaaaggcta ttttcttttt ttttttcttt 60

ctttcattcm ttccttcctc tgtttctttc tttcttcctt tcattttttt ttctttttta 120

agagcgagcg gctctgcggt ggcggtttgg ggtgggcgcc gccgaggtga ggtcgtctcg 180

cctcccgcgc gccggtagat tggttgtttc att atg gat gga ggg gat gat ggt  234
                                     Met Asp Gly Gly Asp Asp Gly
                                      1               5

aac ctt att atc aaa aag agg ttt gtg tct gag gca gaa cta gat gaa   282
Asn Leu Ile Ile Lys Lys Arg Phe Val Ser Glu Ala Glu Leu Asp Glu
        10                  15                  20

cgg cgc aaa agg agg caa gaa gaa tgg gag aaa gtt cga aaa cct gaa   330
Arg Arg Lys Arg Arg Gln Glu Glu Trp Glu Lys Val Arg Lys Pro Glu
    25                  30                  35

gat cca gaa gaa tgt cca gag gag gtt tat gac cct cga tct cta tat   378
Asp Pro Glu Glu Cys Pro Glu Glu Val Tyr Asp Pro Arg Ser Leu Tyr
40                  45                  50                  55
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```
gaa agg cta cag gaa cag aag gac agg aag cag cag gag tac gag gaa    426
Glu Arg Leu Gln Glu Gln Lys Asp Arg Lys Gln Gln Glu Tyr Glu Glu
                60                  65                  70

cag ttc aaa ttc aaa aac atg gta aga ggc tta gat gaa gat gag acc    474
Gln Phe Lys Phe Lys Asn Met Val Arg Gly Leu Asp Glu Asp Glu Thr
            75                  80                  85

aac ttc ctt gat gag gtt tct cga cag cag gaa cta ata gaa aag caa    522
Asn Phe Leu Asp Glu Val Ser Arg Gln Gln Glu Leu Ile Glu Lys Gln
        90                  95                  100

cga aga gaa gaa gaa ctg aaa gaa ctg aag gaa tac aga aat aac ctc    570
Arg Arg Glu Glu Glu Leu Lys Glu Leu Lys Glu Tyr Arg Asn Asn Leu
    105                 110                 115

aag aag gtt gga att tct caa gag aac aag aag gaa gtg gaa aag aaa    618
Lys Lys Val Gly Ile Ser Gln Glu Asn Lys Lys Glu Val Glu Lys Lys
120                 125                 130                 135

ctg act gtg aag cct ata gaa acc aag aac aag ttc tcc cag gcg aag    666
Leu Thr Val Lys Pro Ile Glu Thr Lys Asn Lys Phe Ser Gln Ala Lys
                140                 145                 150

ctg ttg gca gga gct gtg aag cat aag agc tca gag agt ggc aac agt    714
Leu Leu Ala Gly Ala Val Lys His Lys Ser Ser Glu Ser Gly Asn Ser
            155                 160                 165

gtg aaa aga ctg aaa ccg gac cct gag cca gat gac aag aat caa gag    762
Val Lys Arg Leu Lys Pro Asp Pro Glu Pro Asp Asp Lys Asn Gln Glu
        170                 175                 180

ccc tca tcc tgc aag tct ctc gga aac acc tcc ctg agt ggc ccc tcc    810
Pro Ser Ser Cys Lys Ser Leu Gly Asn Thr Ser Leu Ser Gly Pro Ser
    185                 190                 195

atc cac tgc ccc tct gct gca gta tgt atc ggc atc ctc cca ggc ctg    858
Ile His Cys Pro Ser Ala Ala Val Cys Ile Gly Ile Leu Pro Gly Leu
200                 205                 210                 215

ggt gcc tac tct ggg agc agc gac tcc gag tcc agc tca gac agc gaa    906
Gly Ala Tyr Ser Gly Ser Ser Asp Ser Glu Ser Ser Ser Asp Ser Glu
                220                 225                 230

ggc acc atc aat gcc acc gga aag att gtc tcc tcc atc ttc cga acc    954
Gly Thr Ile Asn Ala Thr Gly Lys Ile Val Ser Ser Ile Phe Arg Thr
            235                 240                 245
```

aac acc ttc ctc gag gcc ccc tagtttctcc gtccctacac agggagctcc 1005
Asn Thr Phe Leu Glu Ala Pro
250

tccccaaggg tagatcggac cgttcatgct gcctataggc attatgtccc tcaaaaaaa 1065

actcctttgc ctgcatcctg tgtacaacat gacattttta accaatccaa tctaaaatg 1125

tgccagaatc cacctgtggc ccgaatcgtg tttggttcct ctttctactc cactgcagat 1185

gaccaaacct gtcccgctgc cactttcctc actgatattg ggaggagggc aaggcccagc 1245

cgaagttcca ctaaaaatgc cccaggagaa taggcaccgg ctggcttgcc aaagggtttg 1305

ggttttattg ctttctgttt tttcttttcc cgacagcaca aagaagtaag ggcagttatt 1365

ggacaggtgt tatttaaaca ttctattgta aatgaatgtg ttgtttggtt ctactgcatt 1425

gtggagcatg cgggggaaga gaactgaccc aggtaatgaa atggagccct tccctggaac 1485

taaccagtcc ttgatgttgt gtgactaagt aaagatgata aaccccatct gctgggggtg 1545

tcacttcaca ctcggcatgc attgtgaaag ctttccatac ccttggccat tccctctctc 1605

ctctctctcc aaccccattt atgcaggaag ggactgctaa caagaacgct tccatctcaa 1665

accttttctc tgcctgggaa attattttat gtttgttttt gaaataaagg atttagttta 1725

agattctaaa ttttagagaa acaaacgtag gccttgttta ctaatagcca gacatcagaa 1785

ctgcaggtag gtatgttaat gagatgactt atttctggca gctcctggaa tcctaatatt 1845

gtaaatgagt gggacacact tgcatattgt gaccattcta ttgaggccct ctctgtttaa 1905

tgcatattat acttgtgctt ttaactgtgg aatctatttc taacctaaag gtgctgccct 1965

agtacttttc tttgctgcct ctgctgctct ttttcctttc caaacagcaa ctctgaggcc 2025

atgagcagcc aaaaactaga ggtactgctc cacctcgtct cataaaggga aacgggctca 2085

tcccttggat tctggaggag ggagagggag atggtgtgga ggcctcgagg acagagatag 2145

acatgagctt tgacaacaat ctgtaggctc tcctgcttta gaataagcat gtaccattct 2205

ttatccattc cccttattcc tacatcaatt gtttttactt tcttgggtgt gagactgagt 2265

gagacacaca caaatgtgt tgacactgtg atgccggcag gcagagcagc tactgacttt 2325

FIGURE 1 (CONT'D)

gaacatgggc agagaggcc[illegible] ctggatctca tccagcccac tcctttttccc cttccagtac 2385

agtgacactc tggtgcccat tggcagatgg cgacttccct gcacccataa ctgatgcttt 2445

gtgaattctt cctcctttttc agaactactc tgtgctaatt gttctgccag tatgggcgca 2505

tcagctccat cctgacaaac aagacattta ggtaaaactt tgtaggcacc ttctgcttct 2565

ctgcttcatt gttcctgtga tagtcctgtt gttattacag catgtaccca aaacagcctc 2625

acattgttac aggaggcagg ccaggacatc aaagtcatca tctttatgtg gcatgactct 2685

taagaggcca ttactgtatc tcatggcctc ttgatgtgga aagaagttga cagagggttg 2745

cagggtttaa aaacatccat taacatgaaa gctaataaac ctgtcagaga acaaaaaaaa 2805

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 2850

FIGURE 2

Nucleotide and Amino Acid Sequences of Plasmolipin Like Protein (PLP)

```
cgtccggagc ctgggggaaa agcggcgcgg gagccggcac ccaccgctgg aggggcggcg  60

acggcggccg tagcgacctc gggaggcaag cggagccgcc atg gcc gag ttc ccg   115
                                            Met Ala Glu Phe Pro
                                             1               5

tcg aaa gtt agc acg cgg acc agc agt cct gcg cag ggc gcc gaa gcc   163
Ser Lys Val Ser Thr Arg Thr Ser Ser Pro Ala Gln Gly Ala Glu Ala
                 10                  15                  20

tcg gtg tcg gcg ctg cgc ccg gac ctg ggc ttc gtg cgc tcc cgc ctc   211
Ser Val Ser Ala Leu Arg Pro Asp Leu Gly Phe Val Arg Ser Arg Leu
```

```
        25                   30                   35

ggg gcg ctc atg ctg ctg cag ctg gtg ctg ggg ctg ctg gtg tgg gcg   259
Gly Ala Leu Met Leu Leu Gln Leu Val Leu Gly Leu Leu Val Trp Ala
        40                  45                  50

ctg att gcg gac acc ccg tac cac ctg tat ccg gcc tat ggc tgg gtg   307
Leu Ile Ala Asp Thr Pro Tyr His Leu Tyr Pro Ala Tyr Gly Trp Val
    55                  60                  65

atg ttc gtc gct gtc ttc ctc tgg ctg gtg aca atc gtc ctc ttc aac   355
Met Phe Val Ala Val Phe Leu Trp Leu Val Thr Ile Val Leu Phe Asn
70                  75                  80                  85

ctc tac ctg ttt cag ctg cac atg aag ttg tac atg gtt ccc tgg cca   403
Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr Met Val Pro Trp Pro
                90                  95                  100

ctg gtg tta atg atc ttt aac atc agc gcc acc gtt ctc tac atc acc   451
Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr
            105                 110                 115

gcc ttc atc gcc tgc tct gcg gca gtt gac ctg aca tcc ctg agg ggc   499
Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly
        120                 125                 130

acc cgg cct tat aac cag cgc gcg gct gcc tcg ttc ttt gcg tgt ttg   547
Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu
    135                 140                 145

gtg atg atc gcc tat gga gtg agt gcc ttc ttc agc tac cag gcc tgg   595
Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp
150                 155                 160                 165

cga gga gta ggc agc aat gcg gcc acc agt cag atg gct ggc ggc tat   643
Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly Tyr
                170                 175                 180

gcc taa acc acc tgt gcc acg gcc ccc tct ggg gct gaa gcc gcc gct   691
Ala     Thr Thr Cys Ala Thr Ala Pro Ser Gly Ala Glu Ala Ala Ala
            185                 190                 195

ggg tca cag agc agg gtc acc ctg caa gcc tga agc tgg gga gcc ctg   739
Gly Ser Gln Ser Arg Val Thr Leu Gln Ala     Ser Trp Gly Ala Leu
        200                 205                 210

cgt gga gtc agc cca acagggactg catttgctcc tctctgcccg tcagacataa   794
Arg Gly Val Ser Pro
```

215

gctctcacag cgctaaggaa gcaggcccag gctggcaggc atctcggctt gcaggaggcc 854

aactgctgag acctcttctc catcccccctt attcagtgga agatgacggg ggatctgagg 914

ctgtgtctct gccttgtctt tagaggactt cagcgtccaa gactggggcc caccccttctc 974

accagcacta aatgcactaa caaggactcc agacctgcag ccccagaccc gccgtagtat 1034

aagcctaaca agcaacacgt agcaccttag tctttgttcc aggagagctg agcaagctgg 1094

tgaaaccact ctccttcctt taaacaccgt ttcaaccaac ctctccctgg agccaacctg 1154

taaaaagtgg gttgattgct gacagcatgg tcttccctcc ctgcatttca gacataccag 1214

ttactgaaag caaatcagtt ttaagtgatt tctcagtgct gaaaagcctg tccaggtttc 1274

cttccctttc ccaagcctct ctctgtaata ctcccttgg gcgaagctaa catcggtgcc 1334

tccccgacct tgctgactag gcacatggga cgcaaaggag ggagggaagc aaggccttgc 1394

ctggcgagtt gtcatgtggt tggtggtgac tgttttattt tttttaataa aaataaagat 1454

gagagaaatt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1514

aa 1516

FIGURE 3

Nucleotide and Amino [illegible]d Sequences
of ORPH-PPAR (PPAR)

```
gtgctgtgag gggcttcggg accttggggc agctcctgag ttcagacaga gttcaggaag  60

ggagacaggg gcacagagag acagaggttc atggactgag gcaaaggctg ggccaggctc 120

agcaacccag gcctcccgca ggcaggcaga ggctgccctg taaccc atg gag acc    175
                                                   Met Glu Thr
                                                    1

aga cca aca gct ctg atg agc tcc aca gtg gct gca gct gcg cct gca   223
Arg Pro Thr Ala Leu Met Ser Ser Thr Val Ala Ala Ala Ala Pro Ala
    5                   10                  15

gct ggg gct gcc tcc agg aag gag tct cca ggc aga tgg ggc ctg ggg   271
Ala Gly Ala Ala Ser Arg Lys Glu Ser Pro Gly Arg Trp Gly Leu Gly
20                  25                  30                  35

gag gat ccc aca ggc gtg agc ccc tcg ctc cag tgc cgc gtg tgc gga   319
Glu Asp Pro Thr Gly Val Ser Pro Ser Leu Gln Cys Arg Val Cys Gly
                40                  45                  50

gac agc agc agc ggg aag cac tat ggc atc tat gcc tgc aac ggc tgc   367
Asp Ser Ser Ser Gly Lys His Tyr Gly Ile Tyr Ala Cys Asn Gly Cys
            55                  60                  65

agc ggc ttc ttc aag agg agc gta cgg cgg agg ctc atc tac agg tgc   415
Ser Gly Phe Phe Lys Arg Ser Val Arg Arg Arg Leu Ile Tyr Arg Cys
        70                  75                  80

cag gtg ggg gca ggg atg tgc ccc gtg gac aag gcc cac cgc aac cag   463
Gln Val Gly Ala Gly Met Cys Pro Val Asp Lys Ala His Arg Asn Gln
    85                  90                  95

tgc cag gcc tgc cgg ctg aag aag tgc ctg cag gcg ggg atg aac cag   511
Cys Gln Ala Cys Arg Leu Lys Lys Cys Leu Gln Ala Gly Met Asn Gln
100                 105                 110                 115

gac gcc gtg cag aac gag cgc cag ccg cga agc aca gcc cag gtc cac   559
Asp Ala Val Gln Asn Glu Arg Gln Pro Arg Ser Thr Ala Gln Val His
                120                 125                 130
```

```
ctg gac agc atg gag tcc aac act gag tcc cgg ccg gag tcc ctg gtg    607
Leu Asp Ser Met Glu Ser Asn Thr Glu Ser Arg Pro Glu Ser Leu Val
            135                 140                 145

gct ccc ccg gcc ccg gca ggg cgc agc cca cgg ggc ccc aca ccc atg    655
Ala Pro Pro Ala Pro Ala Gly Arg Ser Pro Arg Gly Pro Thr Pro Met
        150                 155                 160

tct gca gcc aga gcc ctg ggc cac cac ttc atg gcc agc ctt ata aca    703
Ser Ala Ala Arg Ala Leu Gly His His Phe Met Ala Ser Leu Ile Thr
    165                 170                 175

gct gaa acc tgt gct aag ctg gag cca gag gat gct gat gag aat att    751
Ala Glu Thr Cys Ala Lys Leu Glu Pro Glu Asp Ala Asp Glu Asn Ile
180                 185                 190                 195

gat gtc acc agc aat gac cct gag ttc ccc tcc tct cca tac tcc tct    799
Asp Val Thr Ser Asn Asp Pro Glu Phe Pro Ser Ser Pro Tyr Ser Ser
                200                 205                 210

tcc tcc ccc tgc ggc ctg gac agc atc cat gag acc tcg gct cgc cta    847
Ser Ser Pro Cys Gly Leu Asp Ser Ile His Glu Thr Ser Ala Arg Leu
            215                 220                 225

ctc ttc atg gcc gtc aag tgg gcc aag aac ctg cct gtg ttc tcc agc    895
Leu Phe Met Ala Val Lys Trp Ala Lys Asn Leu Pro Val Phe Ser Ser
        230                 235                 240

ctg ccc ttc cgg gat cag gta cct acc ggc ctg cct gct ggg gag cta    943
Leu Pro Phe Arg Asp Gln Val Pro Thr Gly Leu Pro Ala Gly Glu Leu
    245                 250                 255

ggc tgg gct ggg gtc agg cgg ccc act cga gtc aac cag aca ggg cac    991
Gly Trp Ala Gly Val Arg Arg Pro Thr Arg Val Asn Gln Thr Gly His
260                 265                 270                 275

aca cat ccc cac gcc agt atg aat gca cac agc ttg gat ggt gat ggc    1039
Thr His Pro His Ala Ser Met Asn Ala His Ser Leu Asp Gly Asp Gly
                280                 285                 290

tgg gga cac aca tac ctc tgattcagcg atggctgggg tgcatctcag           1087
Trp Gly His Thr Tyr Leu
            295

ggatggtgac ggtgggggtg catgcatctc tggcacaggg atgatggtcg gggtgcacac 1147

ctaggagatg atgatggcta gggacctaca gggcccaggg tcttcttaag ttctggaaga 1207
```

ccctcaggcc ctgcagacat tctgtgggta acaagtgacc tgcacaccct gaacaggctg 1267

agtggctgac tctaggcccc cttggagcac aagtgcctac gacttcaggg cttgcatttt 1327

agttcaatct ctccagctct gggccatccc tctcggcttc taatgggcaa gcagatcttt 1387

caggaaaacc aggaggagag gcatgaggag ggtttgaggc cctcagccag tctgtgtgct 1447

ggggtggagc aactcagaag agtcaggcca caccacttga atacactcaa cttaggacac 1507

tcatgaggca tgtctctgag gctgcccaac ttccaatggc tctgggcgtt cctaaatgtc 1567

ccagctgcag ctctggatgg aacccagtgt ctcagatgat aggcagctga gccggatggt 1627

gccaaatccc agagctctga gcctctggct gatgtcagga gagcattctc gggtcccagg 1687

acagcacttc cattccttgg gtgcctgaga tggtggcaga ggctccagac tgagccagag 1747

aagctgtgtg tctgccataa caggcacccc tgtctgagca caggtgatcc tgctggaaga 1807

ggcgtggagt gaactctttc tcctcggggc catccagtgg tctctgcctc tggacagctg 1867

tcctctgctg gcaccgcccg aggcctctgc tgccggtggt gcccagggcc ggctcacgct 1927

ggccagcatg gagacgcgtg tcctgcagga aactatctct cggttccggg cattggcggt 1987

ggaccccacg gagtttgcct gcatgaaggc cttggtcctc ttcaagccag agacgcgggg 2047

cctgaaggat cctgagcacg tagaggcctt gcaggaccag tcccaagtga tgctgagcca 2107

gcacagcatt ctagaattaa gcggccgctg aattctaggt taagatggcc cttgacattg 2167

agcaggtctt 2177

FIGURE 4

NT2 Like Protein (NTPL) Gene Fragment Sequence

ACTGNCAGGAACTCCTGCCACCGCCACCGGCTCCCATGGCCCACATACCCAGTGGGGGTGCCCCAGCAGCGGGGGCAGCC
CCCATGGGCCCCCAGTATTGCGTGTGCAAGGTGGAGCTGTCAGTGAGTGGCCAGAACCTACTGGACCGGGATGTTACCTC
CAAGTCCGACCCCTTCTGTGTCCTCTTTACAGAGAACAATGGCAGATGGATCGAG

Figure 5 - seven-transmembrane protein

DNA

GAATTCCCACAAAGGAGTCCAGGGTCTCGCTCTGTCACACAGGCTGGAGTGC
AGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTC
TCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAG
TGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGT
TCCTGCTGAGTCTGCTCTTCCTGGTCCAAGCCAGCGGAACCAGACACACAGG
AGCAGCCTCCACTACAAACCCACACCAGACCTGCGCATCTCCATCGAGAACT
CCGAAGAGGCCCTCACAGTCCATGCCCCTTTCCCTGCAGCCCACCCTGCTTCC
CGATCCTTCCCTGACCCCAGGGGCCTCTACCACTTCTGCCTCTACTGGAACCG
ACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTG
ACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCA
GGGCCCCCCGCTGTTAGCCACTTCTGTCACCTCCTGGTGGAGCCCTCAGAACA
TCAGCCTGCCCAGTGCCGCCAGCTTCACCTTCTCCTTCCACAGTCCTCCCCAC
ACGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTCAAAAGGGACCTCC
AGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTC
GGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCT
GTGAGATTCATGGGGGACATGGTGTCCTTCGAGGAGGACCGGATCAACGCCA
CGGTGTGGAAGCTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTC
CCGGCAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCT
CGAACACTCTTCCAGAGGACGAAAGGCCGGAGGGGGGAGGCTGAGAAGAGA
CTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAATTCCA
GCCACGTCCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT
AGCCAACCTCACGGAGCCCGTGGTGCTCACCTTCCAGCACCAGCTACAGCCG
AAGAATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCCACATTGAGCA
GCCCGGGGCATTGGAGCAGTGCTGGGTGTGAGACCGTCAGGAGAGAAACCC
AAACATCCTGCTTCTGCAACCACTTGACCTACTTTGCAGTGCTGATGGTCTCC
TCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCCTCCTCTCCTACG
TGGGCTGTGTCGTCTCTGCCCTGGCCTGCCTTGTCACCATTGCCGCCTACCTCT
GCTCCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCT
GCTGGCCGTCTTCCTGCTGGACACGAGCTTCCTGCTCAGCGAGCCGGTGGCCC
TGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCCTGCACTTCTCC
CTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACT
CGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCG
CCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGAT
GTGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCG
TCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACC
AACCTGGGCCTCTTCAGCCTGGTGTTTCTGTTCAACATGGCCATGCTAGCCAC
CATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACAT
GTGCTGACACTGCTGGGCCTCAGCCTGGTCCTTGGCCTGCCCTGGGCCTTGAT
CTTCTTCTCCTTTGCTTCTGGCACCTTCCAGCTTGTCGTCCTCTACCTTTTCAG
CATCATCACCTCCTTCCAAGGCTTCCTCATCTTCATCTGGTACTGGTCCATGC

GGCTGCAGGCCCGGGGTGGCCCCTCCCCTCTGAAGAGCAACTCAGACAGCGC
CAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCC
AGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCC
TGTGGCCCCCGAGCCAGGCCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGA
AAGCCCAACGACCATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCG
GGCTGGGCTTTTGAATTGGCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCA
CGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTGTCCCCACATCTG
TCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTGGGCCCAGCCCT
CATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATCCT
GTGCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTC
ACCCTGAGGGCACTCTGCATCCTCTGTCATTTTAACCTCAGGTGGCACCCAGG
GCGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGA
GGCCCTTTGCCAGGAGCACAGCAGCAGCTCGCCTACCTCTGAGCCCAGGCCC
CCTCCCTCCCTCAGCCCCCCAGTCCTCCCTCCATCTTCCCTGGGGTTCTCCTCC
TCTCCCAGGGCCTCCTTGCTCCTTCGTTCACAGCTGGGGGTCCCCGATTCCAA
TGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATG
TTTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCAGGCTCGGTACCGATG
CGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATT
GCCCTTGCTCACCCTGACCAAGCACACGCCTCAGAGGGGCCCTCAGCCTCTC
CTGAAGCCCTCTTGTGGCAAGAACTGTGGACCATGCCAGTCCCGTCTGGTTTC
CATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA
GAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTCCAGG
CGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTA
GATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACT
CCTCCTGCCAACATTCAGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTC
CTGGAGCTACAGGGACAGGGAGCCATCATTCCTRCCTGGGAATCCTGGAAGA
CTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGAAGATGGGAAGGATGTTC
TTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTACATGTTCAT
TGTAGAGAATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAATC
AGCTGTTGTAATCGCCTARCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAATAAAAAAAAAAAA

protein

MCELKRDLQLLSQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFE
EDRINATVWKLQPTAGLQDLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKGRRGEA
EKRLLLVDFSSQALFQDKNSSHVLGEKVLGIVVQNTKVANLTEPVVLTFQHQLQ
PKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCFCNHLTYFAVLMVSS
VEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRRKPRDYTIKVHMNLLLA
VFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLEGYNLYRLVVEV
FGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMC
WIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLLGLSL
VLGLPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKS
NSDSARLPISSGSTSSSRI